

Please replace the paragraph beginning at page 62, line 4, with the following rewritten paragraph:

3
The genetic map locations of SEQ ID NO:8-14 are described in The Invention as ranges, or intervals, of human chromosomes. More than one map location is reported for SEQ ID NO:8-14, indicating that previously mapped sequences having similarity, but not complete identity, to SEQ ID NO:8-14 were assembled into their respective clusters. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site at ncbi.nlm.nih.gov/genemap, can be employed to determine if previously identified disease genes map within or in proximity to the intervals indicated above.

IN THE CLAIMS

~~Please cancel claims 210, 218, 227 without prejudice or disclaimer.~~

Please amend claims 205, 213, 215-217, 224-226, 229-231 as follows.

For the Examiner's convenience, all pending claims are listed below. Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "VERSION WITH MARKINGS TO SHOW CHANGES MADE."

205. (Once Amended) An isolated polypeptide comprising an amino acid sequence of SEQ ID NO:12.

206. A composition comprising a polypeptide of claim 205 and a pharmaceutically acceptable excipient.

207. A composition of claim 206, wherein the polypeptide comprises an amino acid sequence of SEQ ID NO:12.

§4 208. A method for treating a disease or condition associated with decreased expression of functional INTRA, comprising administering to a patient in need of such treatment the composition of claim 206.

209. A method of screening for a compound that specifically binds to the polypeptide of claim 205, the method comprising:

- a) combining the polypeptide of claim 205 with at least one test compound under suitable conditions, and
- b) detecting binding of the polypeptide of claim 205 to the test compound, thereby identifying a compound that specifically binds to the polypeptide of claim 205.

211. An isolated polynucleotide encoding a polypeptide comprising an amino acid sequence of SEQ ID NO:12.

§5 212. An isolated polynucleotide of claim 211 comprising a polynucleotide sequence of SEQ ID NO:64.

213. (Once Amended) A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 211.

214. A cell transformed with a recombinant polynucleotide of claim 213.

215. (Once Amended) A method of producing a polypeptide comprising an amino acid sequence of SEQ ID NO:12, the method comprising:

- a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide of claim 211, and
- b) recovering the polypeptide so expressed.

216. (Once Amended) The method of claim 215, wherein the polypeptide comprises an amino acid sequence of SEQ ID NO:12.

217. (Once Amended) An isolated polynucleotide selected from the group consisting of:

- a) a polynucleotide comprising a polynucleotide sequence of SEQ ID NO:64,
- b) a polynucleotide completely complementary to a polynucleotide of a), and
- c) an RNA equivalent of a)-b).

219. A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 217, the method comprising:

- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and
- b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

220. A method of claim 219, wherein the probe comprises at least 60 contiguous nucleotides.

221. A method of detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 217, the method comprising:

- a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
- b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

222. A method of screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 212, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

223. A method of assessing toxicity of a test compound, the method comprising:

- a) treating a biological sample containing nucleic acids with the test compound,
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 217 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 217 or fragment thereof,
- c) quantifying the amount of hybridization complex, and
- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference

B6
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in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

224. A microarray wherein at least one element of the microarray is a polynucleotide of claim 217.

225. (Once Amended) A method of generating an expression profile of a sample which contains polynucleotides, the method comprising:

- a) labeling the polynucleotides of the sample,
- b) contacting the microarray of claim 224 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and
- c) quantifying the expression of the polynucleotides in the sample.

B6
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226. (Once Amended) An array comprising different nucleic acids affixed in distinct physical locations on a solid substrate, wherein at least one of said nucleic acids comprises a first polynucleotide sequence completely complementary to a target polynucleotide, and wherein said target polynucleotide is a polynucleotide of claim 217.

228. An array of claim 226, which is a microarray.

229. (Once Amended) An array of claim 226, further comprising said target polynucleotide hybridized to a nucleic acid comprising said first polynucleotide sequence.

B7

230. (Once Amended) An array of claim 226, wherein a linker joins at least one of said nucleic acids to said solid substrate.

231. (Once Amended) An array of claim 226, wherein each distinct physical location on the substrate contains multiple nucleic acids, and the multiple nucleic acids at any single distinct physical location have the same sequence, and each distinct physical location on the substrate contains nucleic

acids having a sequence which differs from the sequence of nucleic acids at another distinct physical location on the substrate.
